

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ryals, John
Friedrich, Leslie
Uknes, Scott
Molina, Antonio
Ruess, Wilhelm
Knauf-Beiter, Gertrude
Kung, Ruth
Kessmann, Helmut
Oostendorp, Michael
- (ii) TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
- (iii) NUMBER OF SEQUENCES: 32
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Novartis Corporation
(B) STREET: 3054 Cornwallis Road
(C) CITY: Research Triangle Park
(D) STATE: North Carolina
(E) COUNTRY: USA
(F) ZIP: 27709
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/761,543
(B) FILING DATE: 6-DEC-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/034,378
(B) FILING DATE: 27-DEC-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/034,379
(B) FILING DATE: 27-DEC-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/034,382
(B) FILING DATE: 27-DEC-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/034,730
(B) FILING DATE: 10-JAN-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/035,021
(B) FILING DATE: 10-JAN-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/035,022

(B) FILING DATE: 10-JAN-1997

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/035,024
(B) FILING DATE: 10-JAN-1997

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/875,015
(B) FILING DATE: 16-JUL-1997

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Meigs, J. Timothy
(B) REGISTRATION NUMBER: 38,241
(C) REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (919) 541-8587
(B) TELEFAX: (919) 541-8689

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5655 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: exon
(B) LOCATION: 2787..3347
(D) OTHER INFORMATION: /product= "1st exon of NIM1"

(ix) FEATURE:
(A) NAME/KEY: exon
(B) LOCATION: 3427..4162
(D) OTHER INFORMATION: /product= "2nd exon of NIM1"

(ix) FEATURE:
(A) NAME/KEY: exon
(B) LOCATION: 4271..4474
(D) OTHER INFORMATION: /product= "3rd exon of NIM1"

(ix) FEATURE:
(A) NAME/KEY: exon
(B) LOCATION: 4586..4866
(D) OTHER INFORMATION: /product= "4th exon of NIM1"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGTGATGCAA GTCATGGGAT ATTGCTTTGT GTTAAGTATA CAAAACCATC ACGTGGATAC

60

ATAGTCTTCA AACCAACCAC TAAACAGTAT CAGGTCATAC CAAAGCCAGA AGTGAAGGGT	120
TGGGATATGT CATTGGGTTT AGCGGTAATC GGATTGAACC CTTTCCGGTA TAAAATACAA	180
AGGCTTTTCGC AGTCTCGGCG TATGTGTATG TCTCGGGGTA TCTACCATT T GAATCACAGA	240
ACTTTTATGT GCGAAGTTTT CGATTCTGAT TCGTTTACCT GGAAGAGATT AGAAAAATTTG	300
CGTCTACCAA AAACAGACAG ATTAATTTTT TCCAACCCGA TACAAGTTTC GGGGTTCTTG	360
CATTGGATAT CACGGAACAA CAATGTGATC CGGTTTTGTC TCAAAACCGA AACTTGGTCC	420
TTCTTCCATA CTCCGAAC TC TGATGTTTT TCAGGATTAG TCAGATACGA AGGGAAGCTA	480
GGTGCTATTC GTCAGTGGAC AAACAAAGAT CAAGAAGATG TTCACGAGTT ATGGGTTTTA	540
AAGAGCAGTT TTGAAAAGTC GTGGGTAA GTGAAAGATA TTAAAAGCAT TGGAGTAGAT	600
TTGATTACGT GGACTCCAAG CAACGACGTT GTATTGTTTC GTAGTAGTGA TCGTGGTTGC	660
CTCTACAACA TAAACGCAGA GAAGTTGAAT TTAGTTTATG CAAAAAAGA GGGATCTGAT	720
TGTTCTTTTCG TTTGTTTTCC GTTTTGTCT GATTACGAGA GGGTTGATCT GAACGGAAGA	780
AGCAACGGGC CGACACTTTA AAAAAAAT AAAAAAATG GGCCGACAAA TGCAAACGTA	840
GTTGACAAGG ATCTCAAGTC TCAAGTCTCA ATTGGCTCGC TCATTGTGGG GCATAAATAT	900
ATCTAGTGAT GTTTAATTGT TTTTTATAAG GTAAAAAGGA ATATTGAATT TTGTTTCTTA	960
GGTTTATGTA ATAATACCAA ACATTGTTTT ATGAATATTT AATCTGATTT TTTGGCTAGT	1020
TATTTTATTA TATCAAGGGT TCCTGTTTAT AGTTGAAAAC AGTTACTGTA TAGAAAATAG	1080
TGTCCCAATT TTCTCTCTTA AATAATATAT TAGTTAATAA AAGATATTTT AATATATTAG	1140
ATATACATAA TATCTAAAGC AACACATATT TAGACACAAC ACGTAATATC TTACTATTGT	1200
TTACATATAT TTATAGCTTA CCAATATAAC CCGTATCTAT GTTTTATAAG CTTTATACA	1260
ATATATGTAC GGTATGCTGT CCACGTATAT ATATTCTCCA AAAAAACGC ATGGTACACA	1320
AAATTTATTA AATATTTGGC AATTGGGTGT TTATCTAAAG TTTATCACAA TATTTATCAA	1380
CTATAATAGA TGCTAGAAGA TAAAAAATT ATATCAGATT GATTCAATTA AATTTTATAA	1440
TATATCATTT TAAAAATTA ATTAAAAGAA AACTATTTCA TAAAATTGTT CAAAAGATAA	1500
TTAGTAAAAT TAATTAAATA TGTGATGCTA TTGAGTTATA GAGAGTTATT GTAAATTTAC	1560
TTAAAATCAT ACAAATCTTA TCCTAATTTA ACTTATCATT TAAGAAATAC AAAAGTAAAA	1620
AACGCGGAAA GCAATAATTT ATTTACCTTA TTATAACTCC TATATAAAGT ACTCTGTTTA	1680
TTCAACATAA TCTTACGTTG TTGTATTCAT AGGCATCTTT AACCTATCTT TTCATTTTCT	1740
GATCTCGATC GTTTTCGATC CAACAAAATG AGTCTACCGG TGAGGAACCA AGAGGTGATT	1800
ATGCAGATTC CTTCTTCTTC TCAGTTTCCA GCAACATCGA GTCCGGAAAA CACCAATCAA	1860
GTGAAGGATG AGCCAAATTT GTTTAGACGT GTTATGAATT TGCTTTTACG TCGTAGTTAT	1920
TGAAAAAGCT GATTTATCGC ATGATTCAGA ACGAGAAGTT GAAGGCAAAT AACTAAAGAA	1980

GTCTTTTATA TGTATACAAT AATTGTTTTT AAATCAAATC CTAATTAAAA AAATATATTC	2040
ATTATGACTT TCATGTTTTT AATGTAATTT ATTCCTATAT CTATAATGAT TTTGTTGTGA	2100
AGAGCGTTTT CATTTGCTAT AGAACAAGGA GAATAGTTCC AGGAAATATT CGACTTGATT	2160
TAATTATAGT GTAAACATGC TGAACACTGA AAATTACTTT TTCAATAAAC GAAAAATATA	2220
ATATACATTA CAAAACCTAT GTGAATAAAG CATGAACTT AATATACGTT CCCTTTATCA	2280
TTTTACTTCA AAGAAAATAA ACAGAAATGT AACTTTTCACA TGTAATCTA ATTCTTAAAT	2340
TTAAAAAATA ATATTTATAT ATTTATATGA AAATAACGAA CCGGATGAAA AATAAATTTT	2400
ATATATTTAT ATCATCTCCA AATCTAGTTT GGTTCAGGGG CTTACCGAAC CGGATTGAAC	2460
TTCTCATATA CAAAATTAG CAACACAAAA TGTCTCCGGT ATAAATACTA ACATTTATAA	2520
CCCGAACCGG TTTAGCTTCC TGTTATATCT TTTTAAAAA GATCTCTGAC AAAGATTCCCT	2580
TTCTTGAAA TTTACCGGTT TTGGTGAAAT GTAAACCGTG GGACGAGGAT GCTTCTTCAT	2640
ATCTCACCAC CACTCTCGTT GACTTGACTT GGCTCTGCTC GTCAATGGTT ATCTTCGATC	2700
TTTAACCAAA TCCAGTTGAT AAGGTCTCTT CGTTGATTAG CAGAGATCTC TTTAATTTGT	2760
GAATTTCAAT TCATCGGAAC CTGTTG ATG GAC ACC ACC ATT GAT GGA TTC GCC	2813
Met Asp Thr Thr Ile Asp Gly Phe Ala	
1 5	
GAT TCT TAT GAA ATC AGC AGC ACT AGT TTC GTC GCT ACC GAT AAC ACC	2861
Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val Ala Thr Asp Asn Thr	
10 15 20 25	
GAC TCC TCT ATT GTT TAT CTG GCC GCC GAA CAA GTA CTC ACC GGA CCT	2909
Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln Val Leu Thr Gly Pro	
30 35 40	
GAT GTA TCT GCT CTG CAA TTG CTC TCC AAC AGC TTC GAA TCC GTC TTT	2957
Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser Phe Glu Ser Val Phe	
45 50 55	
GAC TCG CCG GAT GAT TTC TAC AGC GAC GCT AAG CTT GTT CTC TCC GAC	3005
Asp Ser Pro Asp Asp Phe Tyr Ser Asp Ala Lys Leu Val Leu Ser Asp	
60 65 70	
GGC CGG GAA GTT TCT TTC CAC CGG TGC GTT TTG TCA GCG AGA AGC TCT	3053
Gly Arg Glu Val Ser Phe His Arg Cys Val Leu Ser Ala Arg Ser Ser	
75 80 85	
TTC TTC AAG AGC GCT TTA GCC GCC GCT AAG AAG GAG AAA GAC TCC AAC	3101
Phe Phe Lys Ser Ala Leu Ala Ala Ala Lys Lys Glu Lys Asp Ser Asn	
90 95 100 105	
AAC ACC GCC GCC GTG AAG CTC GAG CTT AAG GAG ATT GCC AAG GAT TAC	3149
Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu Ile Ala Lys Asp Tyr	
110 115 120	
GAA GTC GGT TTC GAT TCG GTT GTG ACT GTT TTG GCT TAT GTT TAC AGC	3197
Glu Val Gly Phe Asp Ser Val Val Thr Val Leu Ala Tyr Val Tyr Ser	
125 130 135	
AGC AGA GTG AGA CCG CCG CCT AAA GGA GTT TCT GAA TGC GCA GAC GAG	3245
Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser Glu Cys Ala Asp Glu	
140 145 150	

AAT TGC TGC CAC GTG GCT TGC CGG CCG GCG GTG GAT TTC ATG TTG GAG Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp Phe Met Leu Glu 155 160 165	3293
GTT CTC TAT TTG GCT TTC ATC TTC AAG ATC CCT GAA TTA ATT ACT CTC Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile Thr Leu 170 175 180 185	3341
TAT CAG GTAAAACACC ATCTGCATTA AGCTATGGTT ACACATTCAT GAATATGTTC Tyr Gln	3397
TTACTTGAGT ACTTGATATTT GTATTTTCAG AGG CAC TTA TTG GAC GTT GTA GAC Arg His Leu Leu Asp Val Val Asp 190 195	3450
AAA GTT GTT ATA GAG GAC ACA TTG GTT ATA CTC AAG CTT GCT AAT ATA Lys Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile 200 205 210	3498
TGT GGT AAA GCT TGT ATG AAG CTA TTG GAT AGA TGT AAA GAG ATT ATT Cys Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile 215 220 225	3546
GTC AAG TCT AAT GTA GAT ATG GTT AGT CTT GAA AAG TCA TTG CCG GAA Val Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu 230 235 240	3594
GAG CTT GTT AAA GAG ATA ATT GAT AGA CGT AAA GAG CTT GGT TTG GAG Glu Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu 245 250 255	3642
GTA CCT AAA GTA AAG AAA CAT GTC TCG AAT GTA CAT AAG GCA CTT GAC Val Pro Lys Val Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp 260 265 270 275	3690
TCG GAT GAT ATT GAG TTA GTC AAG TTG CTT TTG AAA GAG GAT CAC ACC Ser Asp Asp Ile Glu Leu Val Lys Leu Leu Leu Lys Glu Asp His Thr 280 285 290	3738
AAT CTA GAT GAT GCG TGT GCT CTT CAT TTC GCT GTT GCA TAT TGC AAT Asn Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn 295 300 305	3786
GTG AAG ACC GCA ACA GAT CTT TTA AAA CTT GAT CTT GCC GAT GTC AAC Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn 310 315 320	3834
CAT AGG AAT CCG AGG GGA TAT ACG GTG CTT CAT GTT GCT GCG ATG CGG His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg 325 330 335	3882
AAG GAG CCA CAA TTG ATA CTA TCT CTA TTG GAA AAA GGT GCA AGT GCA Lys Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala 340 345 350 355	3930
TCA GAA GCA ACT TTG GAA GGT AGA ACC GCA CTC ATG ATC GCA AAA CAA Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile Ala Lys Gln 360 365 370	3978
GCC ACT ATG GCG GTT GAA TGT AAT AAT ATC CCG GAG CAA TGC AAG CAT Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln Cys Lys His 375 380 385	4026

TCT	CTC	AAA	GGC	CGA	CTA	TGT	GTA	GAA	ATA	CTA	GAG	CAA	GAA	GAC	AAA		4074
Ser	Leu	Lys	Gly	Arg	Leu	Cys	Val	Glu	Ile	Leu	Glu	Gln	Glu	Asp	Lys		
		390					395					400					
CGA	GAA	CAA	ATT	CCT	AGA	GAT	GTT	CCT	CCC	TCT	TTT	GCA	GTG	GCG	GCC		4122
Arg	Glu	Gln	Ile	Pro	Arg	Asp	Val	Pro	Pro	Ser	Phe	Ala	Val	Ala	Ala		
	405					410					415						
GAT	GAA	TTG	AAG	ATG	ACG	CTG	CTC	GAT	CTT	GAA	AAT	AGA	G				4162
Asp	Glu	Leu	Lys	Met	Thr	Leu	Leu	Asp	Leu	Glu	Asn	Arg					
420					425					430							
GTATCTATCA	AGTCTTATTT	CTTATATGTT	TGAATTAAAT	TTATGTCCTC	TCTATTAGGA												4222
AACTGAGTGA	ACTAATGATA	ACTATTCTTT	GTGTCGTCCA	CTGTTTAG	TT	GCA	CTT										4278
						Val	Ala	Leu									435
GCT	CAA	CGT	CTT	TTT	CCA	ACG	GAA	GCA	CAA	GCT	GCA	ATG	GAG	ATC	GCC		4326
Ala	Gln	Arg	Leu	Phe	Pro	Thr	Glu	Ala	Gln	Ala	Ala	Met	Glu	Ile	Ala		
				440					445					450			
GAA	ATG	AAG	GGA	ACA	TGT	GAG	TTC	ATA	GTG	ACT	AGC	CTC	GAG	CCT	GAC		4374
Glu	Met	Lys	Gly	Thr	Cys	Glu	Phe	Ile	Val	Thr	Ser	Leu	Glu	Pro	Asp		
			455					460					465				
CGT	CTC	ACT	GGT	ACG	AAG	AGA	ACA	TCA	CCG	GGT	GTA	AAG	ATA	GCA	CCT		4422
Arg	Leu	Thr	Gly	Thr	Lys	Arg	Thr	Ser	Pro	Gly	Val	Lys	Ile	Ala	Pro		
		470					475					480					
TTC	AGA	ATC	CTA	GAA	GAG	CAT	CAA	AGT	AGA	CTA	AAA	GCG	CTT	TCT	AAA		4470
Phe	Arg	Ile	Leu	Glu	Glu	His	Gln	Ser	Arg	Leu	Lys	Ala	Leu	Ser	Lys		
	485					490					495						
ACC	G	GTATGGATT	TCACCCACTT	CATCGGACTC	CTTATCACAA	AAAACAAAAC											4524
Thr																	
500																	
TAAATGATCT	TTAAACATGG	TTTTTGTTACT	TGCTGTCTGA	CCTTGTTTTT	TTTATCATCA												4584
G	TG	GAA	CTC	GGG	AAA	CGA	TTC	TTC	CCG	CGC	TGT	TCG	GCA	GTG	CTC		4629
	Val	Glu	Leu	Gly	Lys	Arg	Phe	Phe	Pro	Arg	Cys	Ser	Ala	Val	Leu		
				505					510					515			
GAC	CAG	ATT	ATG	AAC	TGT	GAG	GAC	TTG	ACT	CAA	CTG	GCT	TGC	GGA	GAA		4677
Asp	Gln	Ile	Met	Asn	Cys	Glu	Asp	Leu	Thr	Gln	Leu	Ala	Cys	Gly	Glu		
				520					525					530			
GAC	GAC	ACT	GCT	GAG	AAA	CGA	CTA	CAA	AAG	AAG	CAA	AGG	TAC	ATG	GAA		4725
Asp	Asp	Thr	Ala	Glu	Lys	Arg	Leu	Gln	Lys	Lys	Gln	Arg	Tyr	Met	Glu		
			535					540					545				
ATA	CAA	GAG	ACA	CTA	AAG	AAG	GCC	TTT	AGT	GAG	GAC	AAT	TTG	GAA	TTA		4773
Ile	Gln	Glu	Thr	Leu	Lys	Lys	Ala	Phe									

TAACTGTTTA TGTCTATCGT TGGCGTCATA TAGTTTCGCT CTCGTTTTG CATCCTGTGT 4986
 ATTATTGCTG CAGGTGTGCT TCAAACAAAT GTTGTAAACAA TTTGAACCAA TGGTATACAG 5046
 ATTTGTAATA TATATTTATG TACATCAACA ATAACCCATG ATGGTGTAC AGAGTTGCTA 5106
 GAATCAAAGT GTGAAATAAT GTCAAATTGT TCATCTGTTG GATATTTTCC ACCAAGAACC 5166
 AAAAGAATAT TCAAGTTCCC TGAACCTCTG GCAACATTCA TGTATATGT ATCTTCCTAA 5226
 TTCTTCCTTT AACCTTTTGT AACTCGAATT ACACAGCAAG TTAGTTTCAG GTCTAGAGAT 5286
 AAGAGAACAC TGAGTGGGCG TGTAAGGTGC ATTCTCCTAG TCAGCTCCAT TGCATCCAAC 5346
 ATTTGTGAAT GACACAAGTT AACAATCCTT TGCACCATT CTGGGTGCAT ACATGGAAAC 5406
 TTCTTCGATT GAAACTTCCC ACATGTGCAG GTGCGTTCGC TGTCACTGAT AGACCAAGAG 5466
 ACTGAAAGCT TTCACAAATT GCCCTCAAAT CTTCTGTTTC TATCGTCATG ACTCCATATC 5526
 TCCGACCACT GGTGATGAGC CAGAGCCAC TGATTTTGAG GGAATTGGGC TAACCATTTC 5586
 CGAGCTTCTG AGTCCTTCTT TTTGATGTCC TTTATGTAGG AATCAAATTC TTCCTTCTGA 5646
 CTTGTGGAT 5655

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Thr Thr Ile Asp Gly Phe Ala Asp Ser Tyr Glu Ile Ser Ser
 1 5 10 15
 Thr Ser Phe Val Ala Thr Asp Asn Thr Asp Ser Ser Ile Val Tyr Leu
 20 25 30
 Ala Ala Glu Gln Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu
 35 40 45
 Leu Ser Asn Ser Phe Glu Ser Val Phe Asp Ser Pro Asp Asp Phe Tyr
 50 55 60
 Ser Asp Ala Lys Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His
 65 70 75 80
 Arg Cys Val Leu Ser Ala Arg Ser Ser Phe Phe Lys Ser Ala Leu Ala
 85 90 95
 Ala Ala Lys Lys Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu
 100 105 110
 Glu Leu Lys Glu Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val
 115 120 125
 Val Thr Val Leu Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro
 130 135 140

Lys 145	Gly	Val	Ser	Glu	Cys 150	Ala	Asp	Glu	Asn	Cys 155	Cys	His	Val	Ala	Cys 160
Arg	Pro	Ala	Val	Asp 165	Phe	Met	Leu	Glu	Val 170	Leu	Tyr	Leu	Ala	Phe 175	Ile
Phe	Lys	Ile	Pro 180	Glu	Leu	Ile	Thr	Leu 185	Tyr	Gln	Arg	His	Leu 190	Leu	Asp
Val	Val	Asp 195	Lys	Val	Val	Ile	Glu 200	Asp	Thr	Leu	Val	Ile 205	Leu	Lys	Leu
Ala	Asn 210	Ile	Cys	Gly	Lys	Ala 215	Cys	Met	Lys	Leu	Leu 220	Asp	Arg	Cys	Lys
Glu 225	Ile	Ile	Val	Lys	Ser 230	Asn	Val	Asp	Met	Val 235	Ser	Leu	Glu	Lys	Ser 240
Leu	Pro	Glu	Glu	Leu 245	Val	Lys	Glu	Ile	Ile 250	Asp	Arg	Arg	Lys	Glu 255	Leu
Gly	Leu	Glu	Val 260	Pro	Lys	Val	Lys	Lys 265	His	Val	Ser	Asn	Val 270	His	Lys
Ala	Leu	Asp 275	Ser	Asp	Asp	Ile	Glu 280	Leu	Val	Lys	Leu	Leu 285	Leu	Lys	Glu
Asp	His 290	Thr	Asn	Leu	Asp	Asp 295	Ala	Cys	Ala	Leu	His 300	Phe	Ala	Val	Ala
Tyr 305	Cys	Asn	Val	Lys	Thr 310	Ala	Thr	Asp	Leu	Leu 315	Lys	Leu	Asp	Leu	Ala 320
Asp	Val	Asn	His	Arg 325	Asn	Pro	Arg	Gly	Tyr 330	Thr	Val	Leu	His	Val 335	Ala
Ala	Met	Arg	Lys 340	Glu	Pro	Gln	Leu	Ile 345	Leu	Ser	Leu	Leu 350	Glu	Lys	Gly
Ala	Ser	Ala 355	Ser	Glu	Ala	Thr	Leu 360	Glu	Gly	Arg	Thr	Ala 365	Leu	Met	Ile
Ala	Lys 370	Gln	Ala	Thr	Met	Ala 375	Val	Glu	Cys	Asn	Asn 380	Ile	Pro	Glu	Gln
Cys 385	Lys	His	Ser	Leu	Lys 390	Gly	Arg	Leu	Cys	Val 395	Glu	Ile	Leu	Glu	Gln 400
Glu	Asp	Lys	Arg	Glu 405	Gln	Ile	Pro	Arg	Asp 410	Val	Pro	Pro	Ser	Phe 415	Ala
Val	Ala	Ala	Asp 420	Glu	Leu	Lys	Met	Thr 425	Leu	Leu	Asp	Leu	Glu 430	Asn	Arg
Val	Ala	Leu 435	Ala	Gln	Arg	Leu	Phe 440	Pro	Thr	Glu	Ala	Gln 445	Ala	Ala	Met
Glu	Ile 450	Ala	Glu	Met	Lys	Gly 455	Thr	Cys	Glu	Phe	Ile 460	Val	Thr	Ser	Leu
Glu 465	Pro	Asp	Arg	Leu	Thr 470	Gly	Thr	Lys	Arg	Thr 475	Ser	Pro	Gly	Val	Lys 480
Ile	Ala	Pro	Phe	Arg	Ile	Leu	Glu	Glu	His	Gln	Ser	Arg	Leu	Lys	Ala

Asn Thr Pro Leu His Leu Ala Cys Glu Gln Gly Cys Leu Ala Ser Val
 145 150 155 160
 Ala Val Leu Thr Gln Thr Cys Thr Pro Gln His Leu His Ser Val Leu
 165 170 175
 Gln Ala Thr Asn Tyr Asn Gly His Thr Cys Leu His Leu Ala Ser Thr
 180 185 190
 His Gly Tyr Leu Ala Ile Val Glu His Leu Val Thr Leu Gly Ala Asp
 195 200 205
 Val Asn Ala Gln Glu Pro Cys Asn Gly Arg Thr Ala Leu His Leu Ala
 210 215 220
 Val Asp Leu Gln Asn Pro Asp Leu Val Ser Leu Leu Leu Lys Cys Gly
 225 230 235 240
 Ala Asp Val Asn Arg Val Thr Tyr Gln Gly Tyr Ser Pro Tyr Gln Leu
 245 250 255
 Thr Trp Gly Arg Pro Ser Thr Arg Ile Gln Gln Gln Leu Gly Gln Leu
 260 265 270
 Thr Leu Glu Asn Leu Gln Met Leu Pro Glu Ser Glu Asp Glu Glu Ser
 275 280 285
 Tyr Asp Thr Glu Ser Glu Phe Thr Glu Asp Glu Leu Pro Tyr Asp Asp
 290 295 300
 Cys Val Phe Gly Gly Gln Arg Leu Thr Leu
 305 310

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Phe Gln Pro Ala Gly His Gly Gln Asp Trp Ala Met Glu Gly Pro
 1 5 10 15
 Arg Asp Gly Leu Lys Lys Glu Arg Leu Val Asp Asp Arg His Asp Ser
 20 25 30
 Gly Leu Asp Ser Met Lys Asp Glu Asp Tyr Glu Gln Met Val Lys Glu
 35 40 45
 Leu Arg Glu Ile Arg Leu Gln Pro Gln Glu Ala Pro Leu Ala Ala Glu
 50 55 60
 Pro Trp Lys Gln Gln Leu Thr Glu Asp Gly Asp Ser Phe Leu His Leu
 65 70 75 80

20					25					30					
Gly	Leu	Asp	Ser	Met	Lys	Asp	Glu	Glu	Tyr	Glu	Gln	Met	Val	Lys	Glu
		35					40					45			
Leu	Arg	Glu	Ile	Arg	Leu	Glu	Pro	Gln	Glu	Ala	Pro	Arg	Gly	Ala	Glu
	50					55					60				
Pro	Trp	Lys	Gln	Gln	Leu	Thr	Glu	Asp	Gly	Asp	Ser	Phe	Leu	His	Leu
	65					70					75				80
Ala	Ile	Ile	His	Glu	Glu	Lys	Ala	Leu	Thr	Met	Glu	Val	Val	Arg	Gln
				85					90					95	
Val	Lys	Gly	Asp	Leu	Ala	Phe	Leu	Asn	Phe	Gln	Asn	Asn	Leu	Gln	Gln
			100					105					110		
Thr	Pro	Leu	His	Leu	Ala	Val	Ile	Thr	Asn	Gln	Pro	Glu	Ile	Ala	Glu
		115					120					125			
Ala	Leu	Leu	Glu	Ala	Gly	Cys	Asp	Pro	Glu	Leu	Arg	Asp	Phe	Arg	Gly
	130					135					140				
Asn	Thr	Pro	Leu	His	Leu	Ala	Cys	Glu	Gln	Gly	Cys	Leu	Ala	Ser	Val
	145					150					155				160
Gly	Val	Leu	Thr	Gln	Pro	Arg	Gly	Thr	Gln	His	Leu	His	Ser	Ile	Leu
				165					170					175	
Gln	Ala	Thr	Asn	Tyr	Asn	Gly	His	Thr	Cys	Leu	His	Leu	Ala	Ser	Ile
			180					185					190		
His	Gly	Tyr	Leu	Gly	Ile	Val	Glu	Leu	Leu	Val	Ser	Leu	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Gln	Glu	Pro	Cys	Asn	Gly	Arg	Thr	Ala	Leu	His	Leu	Ala
	210					215					220				
Val	Asp	Leu	Gln	Asn	Pro	Asp	Leu	Val	Ser	Leu	Leu	Leu	Lys	Cys	Gly
	225					230					235				240
Ala	Asp	Val	Asn	Arg	Val	Thr	Tyr	Gln	Gly	Tyr	Ser	Pro	Tyr	Gln	Leu
				245					250					255	
Thr	Trp	Gly	Arg	Pro	Ser	Thr	Arg	Ile	Gln	Gln	Gln	Leu	Gly	Gln	Leu
			260					265					270		
Thr	Leu	Glu	Asn	Leu	Gln	Met	Leu	Pro	Glu	Ser	Glu	Asp	Glu	Glu	Ser
		275					280					285			
Tyr	Asp	Thr	Glu	Ser	Glu	Phe	Thr	Glu	Asp	Glu	Leu	Pro	Tyr	Asp	Asp
	290					295					300				
Cys	Val	Leu	Gly	Gly	Gln	Arg	Leu	Thr	Leu						
	305					310									

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2011 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..2011

(D) OTHER INFORMATION: /note= "NIM1 cDNA sequence"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 43..1824

(D) OTHER INFORMATION: /product= "NIM1 protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATCTCTTTA ATTTGTGAAT TTCAATTCAT CGGAACCTGT TG ATG GAC ACC ACC	54
Met Asp Thr Thr	
1	
ATT GAT GGA TTC GCC GAT TCT TAT GAA ATC AGC AGC ACT AGT TTC GTC	102
Ile Asp Gly Phe Ala Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val	
5 10 15 20	
GCT ACC GAT AAC ACC GAC TCC TCT ATT GTT TAT CTG GCC GCC GAA CAA	150
Ala Thr Asp Asn Thr Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln	
25 30 35	
GTA CTC ACC GGA CCT GAT GTA TCT GCT CTG CAA TTG CTC TCC AAC AGC	198
Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser	
40 45 50	
TTC GAA TCC GTC TTT GAC TCG CCG GAT GAT TTC TAC AGC GAC GCT AAG	246
Phe Glu Ser Val Phe Asp Ser Pro Asp Asp Phe Tyr Ser Asp Ala Lys	
55 60 65	
CTT GTT CTC TCC GAC GGC CGG GAA GTT TCT TTC CAC CGG TGC GTT TTG	294
Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His Arg Cys Val Leu	
70 75 80	
TCA GCG AGA AGC TCT TTC TTC AAG AGC GCT TTA GCC GCC GCT AAG AAG	342
Ser Ala Arg Ser Ser Phe Phe Lys Ser Ala Leu Ala Ala Ala Lys Lys	
85 90 95 100	
GAG AAA GAC TCC AAC AAC ACC GCC GCC GTG AAG CTC GAG CTT AAG GAG	390
Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu	
105 110 115	
ATT GCC AAG GAT TAC GAA GTC GGT TTC GAT TCG GTT GTG ACT GTT TTG	438
Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu	
120 125 130	
GCT TAT GTT TAC AGC AGC AGA GTG AGA CCG CCG CCT AAA GGA GTT TCT	486
Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser	
135 140 145	
GAA TGC GCA GAC GAG AAT TGC TGC CAC GTG GCT TGC CGG CCG GCG GTG	534
Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val	
150 155 160	
GAT TTC ATG TTG GAG GTT CTC TAT TTG GCT TTC ATC TTC AAG ATC CCT	582
Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro	
165 170 175 180	

GAA TTA ATT ACT CTC TAT CAG AGG CAC TTA TTG GAC GTT GTA GAC AAA Glu Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp Val Val Asp Lys 185 190 195	630
GTT GTT ATA GAG GAC ACA TTG GTT ATA CTC AAG CTT GCT AAT ATA TGT Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile Cys 200 205 210	678
GGT AAA GCT TGT ATG AAG CTA TTG GAT AGA TGT AAA GAG ATT ATT GTC Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile Val 215 220 225	726
AAG TCT AAT GTA GAT ATG GTT AGT CTT GAA AAG TCA TTG CCG GAA GAG Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu Glu 230 235 240	774
CTT GTT AAA GAG ATA ATT GAT AGA CGT AAA GAG CTT GGT TTG GAG GTA Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu Val 245 250 255 260	822
CCT AAA GTA AAG AAA CAT GTC TCG AAT GTA CAT AAG GCA CTT GAC TCG Pro Lys Val Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp Ser 265 270 275	870
GAT GAT ATT GAG TTA GTC AAG TTG CTT TTG AAA GAG GAT CAC ACC AAT Asp Asp Ile Glu Leu Val Lys Leu Leu Leu Lys Glu Asp His Thr Asn 280 285 290	918
CTA GAT GAT GCG TGT GCT CTT CAT TTC GCT GTT GCA TAT TGC AAT GTG Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn Val 295 300 305	966
AAG ACC GCA ACA GAT CTT TTA AAA CTT GAT CTT GCC GAT GTC AAC CAT Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn His 310 315 320	1014
AGG AAT CCG AGG GGA TAT ACG GTG CTT CAT GTT GCT GCG ATG CGG AAG Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg Lys 325 330 335 340	1062
GAG CCA CAA TTG ATA CTA TCT CTA TTG GAA AAA GGT GCA AGT GCA TCA Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala Ser 345 350 355	1110
GAA GCA ACT TTG GAA GGT AGA ACC GCA CTC ATG ATC GCA AAA CAA GCC Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile Ala Lys Gln Ala 360 365 370	1158
ACT ATG GCG GTT GAA TGT AAT AAT ATC CCG GAG CAA TGC AAG CAT TCT Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln Cys Lys His Ser 375 380 385	1206
CTC AAA GGC CGA CTA TGT GTA GAA ATA CTA GAG CAA GAA GAC AAA CGA Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln Glu Asp Lys Arg 390 395 400	1254
GAA CAA ATT CCT AGA GAT GTT CCT CCC TCT TTT GCA GTG GCG GCC GAT Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala Val Ala Ala Asp 405 410 415 420	1302
GAA TTG AAG ATG ACG CTG CTC GAT CTT GAA AAT AGA GTT GCA CTT GCT Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg Val Ala Leu Ala 425 430 435	1350

CAA CGT CTT TTT CCA ACG GAA GCA CAA GCT GCA ATG GAG ATC GCC GAA	1398
Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met Glu Ile Ala Glu	
440 445 450	
ATG AAG GGA ACA TGT GAG TTC ATA GTG ACT AGC CTC GAG CCT GAC CGT	1446
Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp Arg	
455 460 465	
CTC ACT GGT ACG AAG AGA ACA TCA CCG GGT GTA AAG ATA GCA CCT TTC	1494
Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro Phe	
470 475 480	
AGA ATC CTA GAA GAG CAT CAA AGT AGA CTA AAA GCG CTT TCT AAA ACC	1542
Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala Leu Ser Lys Thr	
485 490 495 500	
GTG GAA CTC GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC GAC	1590
Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu Asp	
505 510 515	
CAG ATT ATG AAC TGT GAG GAC TTG ACT CAA CTG GCT TGC GGA GAA GAC	1638
Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala Cys Gly Glu Asp	
520 525 530	
GAC ACT GCT GAG AAA CGA CTA CAA AAG AAG CAA AGG TAC ATG GAA ATA	1686
Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met Glu Ile	
535 540 545	
CAA GAG ACA CTA AAG AAG GCC TTT AGT GAG GAC AAT TTG GAA TTA GGA	1734
Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asn Leu Glu Leu Gly	
550 555 560	
AAT TTG TCC CTG ACA GAT TCG ACT TCT TCC ACA TCG AAA TCA ACC GGT	1782
Asn Leu Ser Leu Thr Asp Ser Thr Ser Ser Thr Ser Lys Ser Thr Gly	
565 570 575 580	
GGA AAG AGG TCT AAC CGT AAA CTC TCT CAT CGT CGT CGG TGA	1824
Gly Lys Arg Ser Asn Arg Lys Leu Ser His Arg Arg Arg *	
585 590	
GACTCTTGCC TCTTAGTGTA ATTTTGTGCTG TACCATATAA TTCTGTTTTTC ATGATGACTG	1884
TAAGTGTGTTA TGTCTATCGT TGGCGTCATA TAGTTTCGCT CTTCGTTTTTG CATCCTGTGT	1944
ATTATGTGCTG CAGGTGTGCT TCAAACAAAT GTTGTAACAA TTTGAACCAA TGGTATACAG	2004
ATTTGTA	2011

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2011 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 - (B) LOCATION: 43..1824
 - (D) OTHER INFORMATION: /product= "altered form of NIM1"
- /note= "Serine residues at amino acid positions 55 and 59 in

wild-type NIM1 gene product have been changed to Alanine residues."

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 205..217

(D) OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATCTCTTTA ATTTGTGAAT TTCAATTCAT CGGAACCTGT TG ATG GAC ACC ACC	54
Met Asp Thr Thr	
1	
ATT GAT GGA TTC GCC GAT TCT TAT GAA ATC AGC AGC ACT AGT TTC GTC	102
Ile Asp Gly Phe Ala Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val	
5 10 15 20	
GCT ACC GAT AAC ACC GAC TCC TCT ATT GTT TAT CTG GCC GCC GAA CAA	150
Ala Thr Asp Asn Thr Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln	
25 30 35	
GTA CTC ACC GGA CCT GAT GTA TCT GCT CTG CAA TTG CTC TCC AAC AGC	198
Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser	
40 45 50	
TTC GAA GCC GTC TTT GAC GCG CCG GAT GAT TTC TAC AGC GAC GCT AAG	246
Phe Glu Ala Val Phe Asp Ala Pro Asp Asp Phe Tyr Ser Asp Ala Lys	
55 60 65	
CTT GTT CTC TCC GAC GGC CGG GAA GTT TCT TTC CAC CGG TGC GTT TTG	294
Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His Arg Cys Val Leu	
70 75 80	
TCA GCG AGA AGC TCT TTC TTC AAG AGC GCT TTA GCC GCC GCT AAG AAG	342
Ser Ala Arg Ser Ser Phe Phe Lys Ser Ala Leu Ala Ala Ala Lys Lys	
85 90 95 100	
GAG AAA GAC TCC AAC AAC ACC GCC GCC GTG AAG CTC GAG CTT AAG GAG	390
Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu	
105 110 115	
ATT GCC AAG GAT TAC GAA GTC GGT TTC GAT TCG GTT GTG ACT GTT TTG	438
Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu	
120 125 130	
GCT TAT GTT TAC AGC AGC AGA GTG AGA CCG CCG CCT AAA GGA GTT TCT	486
Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser	
135 140 145	
GAA TGC GCA GAC GAG AAT TGC TGC CAC GTG GCT TGC CGG CCG GCG GTG	534
Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val	
150 155 160	
GAT TTC ATG TTG GAG GTT CTC TAT TTG GCT TTC ATC TTC AAG ATC CCT	582
Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro	
165 170 175 180	
GAA TTA ATT ACT CTC TAT CAG AGG CAC TTA TTG GAC GTT GTA GAC AAA	630
Glu Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp Val Val Asp Lys	
185 190 195	
GTT GTT ATA GAG GAC ACA TTG GTT ATA CTC AAG CTT GCT AAT ATA TGT	678

Val	Val	Ile	Glu	Asp	Thr	Leu	Val	Ile	Leu	Lys	Leu	Ala	Asn	Ile	Cys	
			200					205					210			
GGT	AAA	GCT	TGT	ATG	AAG	CTA	TTG	GAT	AGA	TGT	AAA	GAG	ATT	ATT	GTC	726
Gly	Lys	Ala	Cys	Met	Lys	Leu	Leu	Asp	Arg	Cys	Lys	Glu	Ile	Ile	Val	
		215					220					225				
AAG	TCT	AAT	GTA	GAT	ATG	GTT	AGT	CTT	GAA	AAG	TCA	TTG	CCG	GAA	GAG	774
Lys	Ser	Asn	Val	Asp	Met	Val	Ser	Leu	Glu	Lys	Ser	Leu	Pro	Glu	Glu	
	230					235					240					
CTT	GTT	AAA	GAG	ATA	ATT	GAT	AGA	CGT	AAA	GAG	CTT	GGT	TTG	GAG	GTA	822
Leu	Val	Lys	Glu	Ile	Ile	Asp	Arg	Arg	Lys	Glu	Leu	Gly	Leu	Glu	Val	
245					250					255					260	
CCT	AAA	GTA	AAG	AAA	CAT	GTC	TCG	AAT	GTA	CAT	AAG	GCA	CTT	GAC	TCG	870
Pro	Lys	Val	Lys	Lys	His	Val	Ser	Asn	Val	His	Lys	Ala	Leu	Asp	Ser	
				265					270					275		
GAT	GAT	ATT	GAG	TTA	GTC	AAG	TTG	CTT	TTG	AAA	GAG	GAT	CAC	ACC	AAT	918
Asp	Asp	Ile	Glu	Leu	Val	Lys	Leu	Leu	Leu	Lys	Glu	Asp	His	Thr	Asn	
			280					285					290			
CTA	GAT	GAT	GCG	TGT	GCT	CTT	CAT	TTC	GCT	GTT	GCA	TAT	TGC	AAT	GTG	966
Leu	Asp	Asp	Ala	Cys	Ala	Leu	His	Phe	Ala	Val	Ala	Tyr	Cys	Asn	Val	
		295					300					305				
AAG	ACC	GCA	ACA	GAT	CTT	TTA	AAA	CTT	GAT	CTT	GCC	GAT	GTC	AAC	CAT	1014
Lys	Thr	Ala	Thr	Asp	Leu	Leu	Lys	Leu	Asp	Leu	Ala	Asp	Val	Asn	His	
	310					315					320					
AGG	AAT	CCG	AGG	GGA	TAT	ACG	GTG	CTT	CAT	GTT	GCT	GCG	ATG	CGG	AAG	1062
Arg	Asn	Pro	Arg	Gly	Tyr	Thr	Val	Leu	His	Val	Ala	Ala	Met	Arg	Lys	
325					330					335					340	
GAG	CCA	CAA	TTG	ATA	CTA	TCT	CTA	TTG	GAA	AAA	GGT	GCA	AGT	GCA	TCA	1110
Glu	Pro	Gln	Leu	Ile	Leu	Ser	Leu	Leu	Glu	Lys	Gly	Ala	Ser	Ala	Ser	
				345					350					355		
GAA	GCA	ACT	TTG	GAA	GGT	AGA	ACC	GCA	CTC	ATG	ATC	GCA	AAA	CAA	GCC	1158
Glu	Ala	Thr	Leu	Glu	Gly	Arg	Thr	Ala	Leu	Met	Ile	Ala	Lys	Gln	Ala	
			360					365					370			
ACT	ATG	GCG	GTT	GAA	TGT	AAT	AAT	ATC	CCG	GAG	CAA	TGC	AAG	CAT	TCT	1206
Thr	Met	Ala	Val	Glu	Cys	Asn	Asn	Ile	Pro	Glu	Gln	Cys	Lys	His	Ser	
		375					380					385				
CTC	AAA	GGC	CGA	CTA	TGT	GTA	GAA	ATA	CTA	GAG	CAA	GAA	GAC	AAA	CGA	1254
Leu	Lys	Gly	Arg	Leu	Cys	Val	Glu	Ile	Leu	Glu	Gln	Glu	Asp	Lys	Arg	
	390					395					400					
GAA	CAA	ATT	CCT	AGA	GAT	GTT	CCT	CCC	TCT	TTT	GCA	GTG	GCG	GCC	GAT	1302
Glu	Gln	Ile	Pro	Arg	Asp	Val	Pro	Pro	Ser	Phe	Ala	Val	Ala	Ala	Asp	
405					410					415					420	
GAA	TTG	AAG	ATG	ACG	CTG	CTC	GAT	CTT	GAA	AAT	AGA	GTT	GCA	CTT	GCT	1350
Glu	Leu	Lys	Met	Thr	Leu	Leu	Asp	Leu	Glu	Asn	Arg	Val	Ala	Leu	Ala	
				425					430					435		
CAA	CGT	CTT	TTT	CCA	ACG	GAA	GCA	CAA	GCT	GCA	ATG	GAG	ATC	GCC	GAA	1398
Gln	Arg	Leu	Phe	Pro	Thr	Glu	Ala	Gln	Ala	Ala	Met	Glu	Ile	Ala	Glu	
			440					445					450			
ATG	AAG	GGA	ACA	TGT	GAG	TTC	ATA	GTG	ACT	AGC	CTC	GAG	CCT	GAC	CGT	1446
Met	Lys	Gly	Thr	Cys	Glu	Phe	Ile	Val	Thr	Ser	Leu	Glu	Pro	Asp	Arg	

455	460	465	
CTC ACT GGT ACG AAG AGA ACA TCA CCG GGT GTA AAG ATA GCA CCT TTC Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro Phe 470 475 480			1494
AGA ATC CTA GAA GAG CAT CAA AGT AGA CTA AAA GCG CTT TCT AAA ACC Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala Leu Ser Lys Thr 485 490 495 500			1542
GTG GAA CTC GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC GAC Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu Asp 505 510 515			1590
CAG ATT ATG AAC TGT GAG GAC TTG ACT CAA CTG GCT TGC GGA GAA GAC Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala Cys Gly Glu Asp 520 525 530			1638
GAC ACT GCT GAG AAA CGA CTA CAA AAG AAG CAA AGG TAC ATG GAA ATA Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met Glu Ile 535 540 545			1686
CAA GAG ACA CTA AAG AAG GCC TTT AGT GAG GAC AAT TTG GAA TTA GGA Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asn Leu Glu Leu Gly 550 555 560			1734
AAT TTG TCC CTG ACA GAT TCG ACT TCT TCC ACA TCG AAA TCA ACC GGT Asn Leu Ser Leu Thr Asp Ser Thr Ser Ser Thr Ser Lys Ser Thr Gly 565 570 575 580			1782
GGA AAG AGG TCT AAC CGT AAA CTC TCT CAT CGT CGT CGG TGA Gly Lys Arg Ser Asn Arg Lys Leu Ser His Arg Arg Arg *			1824
585 590			
GACTCTTGCC TCTTAGTGTA ATTTTGTGCTG TACCATATAA TTCTGTTTTTC ATGATGACTG			1884
TAAGTGTGTTA TGTCTATCGT TGGCGTCATA TAGTTTCGCT CTTCGTTTTG CATCCTGTGT			1944
ATTATGCTG CAGGTGTGCT TCAAACAAAT GTTGTAACAA TTTGAACCAA TGGTATACAG			2004
ATTTGTA			2011

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 594 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Thr Thr Ile Asp Gly Phe Ala Asp Ser Tyr Glu Ile Ser Ser 1 5 10 15
Thr Ser Phe Val Ala Thr Asp Asn Thr Asp Ser Ser Ile Val Tyr Leu 20 25 30
Ala Ala Glu Gln Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu 35 40 45
Leu Ser Asn Ser Phe Glu Ala Val Phe Asp Ala Pro Asp Asp Phe Tyr 50 55 60

Ser Asp Ala Lys Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His
65 70 75 80

Arg Cys Val Leu Ser Ala Arg Ser Ser Phe Phe Lys Ser Ala Leu Ala
85 90 95

Ala Ala Lys Lys Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu
100 105 110

Glu Leu Lys Glu Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val
115 120 125

Val Thr Val Leu Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro
130 135 140

Lys Gly Val Ser Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys
145 150 155 160

Arg Pro Ala Val Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile
165 170 175

Phe Lys Ile Pro Glu Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp
180 185 190

Val Val Asp Lys Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu
195 200 205

Ala Asn Ile Cys Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys
210 215 220

Glu Ile Ile Val Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser
225 230 235 240

Leu Pro Glu Glu Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu
245 250 255

Gly Leu Glu Val Pro Lys Val Lys Lys His Val Ser Asn Val His Lys
260 265 270

Ala Leu Asp Ser Asp Asp Ile Glu Leu Val Lys Leu Leu Leu Lys Glu
275 280 285

Asp His Thr Asn Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala
290 295 300

Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala
305 310 315 320

Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala
325 330 335

Ala Met Arg Lys Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly
340 345 350

Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile
355 360 365

Ala Lys Gln Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln
370 375 380

Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln
385 390 395 400

Glu Asp Lys Arg Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala

	405		410		415										
Val	Ala	Ala	Asp	Glu	Leu	Lys	Met	Thr	Leu	Leu	Asp	Leu	Glu	Asn	Arg
			420					425					430		
Val	Ala	Leu	Ala	Gln	Arg	Leu	Phe	Pro	Thr	Glu	Ala	Gln	Ala	Ala	Met
		435					440					445			
Glu	Ile	Ala	Glu	Met	Lys	Gly	Thr	Cys	Glu	Phe	Ile	Val	Thr	Ser	Leu
	450					455					460				
Glu	Pro	Asp	Arg	Leu	Thr	Gly	Thr	Lys	Arg	Thr	Ser	Pro	Gly	Val	Lys
465					470					475					480
Ile	Ala	Pro	Phe	Arg	Ile	Leu	Glu	Glu	His	Gln	Ser	Arg	Leu	Lys	Ala
				485					490					495	
Leu	Ser	Lys	Thr	Val	Glu	Leu	Gly	Lys	Arg	Phe	Phe	Pro	Arg	Cys	Ser
			500					505					510		
Ala	Val	Leu	Asp	Gln	Ile	Met	Asn	Cys	Glu	Asp	Leu	Thr	Gln	Leu	Ala
		515					520					525			
Cys	Gly	Glu	Asp	Asp	Thr	Ala	Glu	Lys	Arg	Leu	Gln	Lys	Lys	Gln	Arg
	530					535					540				
Tyr	Met	Glu	Ile	Gln	Glu	Thr	Leu	Lys	Lys	Ala	Phe	Ser	Glu	Asp	Asn
545					550					555					560
Leu	Glu	Leu	Gly	Asn	Leu	Ser	Leu	Thr	Asp	Ser	Thr	Ser	Ser	Thr	Ser
				565					570					575	
Lys	Ser	Thr	Gly	Gly	Lys	Arg	Ser	Asn	Arg	Lys	Leu	Ser	His	Arg	Arg
			580					585					590		
Arg	*														

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1597 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1410
 - (D) OTHER INFORMATION: /product= "Altered form of NIM1"
- /note= "N-terminal deletion compared to wild-type NIM1 sequence."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG	GAT	TCG	GTT	GTG	ACT	GTT	TTG	GCT	TAT	GTT	TAC	AGC	AGC	AGA	GTG	48
Met	Asp	Ser	Val	Val	Thr	Val	Leu	Ala	Tyr	Val	Tyr	Ser	Ser	Arg	Val	
1				5					10					15		
AGA	CCG	CCG	CCT	AAA	GGA	GTT	TCT	GAA	TGC	GCA	GAC	GAG	AAT	TGC	TGC	96
Arg	Pro	Pro	Pro	Lys	Gly	Val	Ser	Glu	Cys	Ala	Asp	Glu	Asn	Cys	Cys	

			20				25				30							
CAC His	GTG Val	GCT Ala 35	TGC Cys	CGG Arg	CCG Pro	GCG Ala	GTG Val 40	GAT Asp	TTC Phe	ATG Met	TTG Leu	GAG Glu 45	GTT Val	CTC Leu	TAT Tyr	144		
TTG Leu	GCT Ala 50	TTC Phe	ATC Ile	TTC Phe	AAG Lys	ATC Ile 55	CCT Pro	GAA Glu	TTA Leu	ATT Ile 60	ACT Thr	CTC Leu	TAT Tyr	CAG Gln	AGG Arg	192		
CAC His 65	TTA Leu	TTG Leu	GAC Asp	GTT Val	GTA Val 70	GAC Asp	AAA Lys	GTT Val	GTT Val 75	ATA Ile	GAG Glu	GAC Asp	ACA Thr	TTG Leu	GTT Val 80	240		
ATA Ile	CTC Leu	AAG Lys	CTT Leu	GCT Ala 85	AAT Asn	ATA Ile	TGT Cys	GGT Gly	AAA Lys 90	GCT Ala	TGT Cys	ATG Met	AAG Lys	CTA Leu 95	TTG Leu	288		
GAT Asp	AGA Arg	TGT Cys	AAA Lys 100	GAG Glu	ATT Ile	ATT Ile	GTC Val	AAG Lys 105	TCT Ser	AAT Asn	GTA Val	GAT Asp	ATG Met 110	GTT Val	AGT Ser	336		
CTT Leu	GAA Glu	AAG Lys 115	TCA Ser	TTG Leu	CCG Pro	GAA Glu	GAG Glu 120	CTT Leu	GTT Val	AAA Lys	GAG Glu 125	ATA Ile	ATT Ile	GAT Asp	AGA Arg	384		
CGT Arg	AAA Lys 130	GAG Glu	CTT Leu	GGT Gly	TTG Leu	GAG Glu 135	GTA Val	CCT Pro	AAA Lys	GTA Val 140	AAG Lys	AAA Lys	CAT His	GTC Val	TCG Ser	432		
AAT Asn 145	GTA Val	CAT His	AAG Lys	GCA Ala	CTT Leu 150	GAC Asp	TCG Ser	GAT Asp	GAT Asp 155	ATT Ile	GAG Glu	TTA Leu	GTC Val	AAG Lys	TTG Leu 160	480		
CTT Leu	TTG Leu	AAA Lys	GAG Glu	GAT Asp 165	CAC His	ACC Thr	AAT Asn	CTA Leu	GAT Asp 170	GAT Asp	GCG Ala	TGT Cys	GCT Ala	CTT Leu 175	CAT His	528		
TTC Phe	GCT Ala	GTT Val	GCA Ala 180	TAT Tyr	TGC Cys	AAT Asn	GTG Val	AAG Lys 185	ACC Thr	GCA Ala	ACA Thr	GAT Asp	CTT Leu 190	TTA Leu	AAA Lys	576		
CTT Leu	GAT Asp	CTT Leu 195	GCC Ala	GAT Asp	GTC Val	AAC Asn	CAT His 200	AGG Arg	AAT Asn	CCG Pro	AGG Arg	GGA Gly 205	TAT Tyr	ACG Thr	GTG Val	624		
CTT Leu	CAT His 210	GTT Val	GCT Ala	GCG Ala	ATG Met	CGG Arg 215	AAG Lys	GAG Glu	CCA Pro	CAA Gln	TTG Leu 220	ATA Ile	CTA Leu	TCT Ser	CTA Leu	672		
TTG Leu 225	GAA Glu	AAA Lys	GGT Gly	GCA Ala	AGT Ser 230	GCA Ala	TCA Ser	GAA Glu	GCA Ala	ACT Thr 235	TTG Leu	GAA Glu	GGT Gly	AGA Arg	ACC Thr 240	720		
GCA Ala	CTC Leu	ATG Met	ATC Ile 245	GCA Ala	AAA Lys	CAA Gln	GCC Ala	ACT Thr 250	ATG Met	GCG Ala	GTT Val	GAA Glu	TGT Cys	AAT Asn 255	AAT Asn	768		
ATC Ile	CCG Pro	GAG Glu	CAA Gln 260	TGC Cys	AAG Lys	CAT His	TCT Ser	CTC Leu 265	AAA Lys	GGC Gly	CGA Arg	CTA Leu	TGT Cys 270	GTA Val	GAA Glu	816		
ATA Ile	CTA Leu	GAG Glu 275	CAA Gln	GAA Glu	GAC Asp	AAA Lys	CGA Arg 280	GAA Glu	CAA Gln	ATT Ile	CCT Pro	AGA Arg 285	GAT Asp	GTT Val	CCT Pro	864		

CCC Pro	TCT Ser	TTT Phe	GCA Ala	GTG Val	GCG Ala	GCC Ala	GAT Asp	GAA Glu	TTG Leu	AAG Lys	ATG Met	ACG Thr	CTG Leu	CTC Leu	GAT Asp	912
290 295 300																
CTT Leu	GAA Glu	AAT Asn	AGA Arg	GTT Val	GCA Ala	CTT Leu	GCT Ala	CAA Gln	CGT Arg	CTT Leu	TTT Phe	CCA Pro	ACG Thr	GAA Glu	GCA Ala	960
305 310 315 320																
CAA Gln	GCT Ala	GCA Ala	ATG Met	GAG Glu	ATC Ile	GCC Ala	GAA Glu	ATG Met	AAG Lys	GGA Gly	ACA Thr	TGT Cys	GAG Glu	TTC Phe	ATA Ile	1008
325 330 335																
GTG Val	ACT Thr	AGC Ser	CTC Leu	GAG Glu	CCT Pro	GAC Asp	CGT Arg	CTC Leu	ACT Thr	GGT Gly	ACG Thr	AAG Lys	AGA Arg	ACA Thr	TCA Ser	1056
340 345 350																
CCG Pro	GGT Gly	GTA Val	AAG Lys	ATA Ile	GCA Ala	CCT Pro	TTC Phe	AGA Arg	ATC Ile	CTA Leu	GAA Glu	GAG Glu	CAT His	CAA Gln	AGT Ser	1104
355 360 365																
AGA Arg	CTA Leu	AAA Lys	GCG Ala	CTT Leu	TCT Ser	AAA Lys	ACC Thr	GTG Val	GAA Glu	CTC Leu	GGG Gly	AAA Lys	CGA Arg	TTC Phe	TTC Phe	1152
370 375 380																
CCG Pro	CGC Arg	TGT Cys	TCG Ser	GCA Ala	GTG Val	CTC Leu	GAC Asp	CAG Gln	ATT Ile	ATG Met	AAC Asn	TGT Cys	GAG Glu	GAC Asp	TTG Leu	1200
385 390 395 400																
ACT Thr	CAA Gln	CTG Leu	GCT Ala	TGC Cys	GGA Gly	GAA Glu	GAC Asp	GAC Asp	ACT Thr	GCT Ala	GAG Glu	AAA Lys	CGA Arg	CTA Leu	CAA Gln	1248
405 410 415																
AAG Lys	AAG Lys	CAA Gln	AGG Arg	TAC Tyr	ATG Met	GAA Glu	ATA Ile	CAA Gln	GAG Glu	ACA Thr	CTA Leu	AAG Lys	AAG Lys	GCC Ala	TTT Phe	1296
420 425 430																
AGT Ser	GAG Glu	GAC Asp	AAT Asn	TTG Leu	GAA Glu	TTA Leu	GGA Gly	AAT Asn	TTG Leu	TCC Ser	CTG Leu	ACA Thr	GAT Asp	TCG Ser	ACT Thr	1344
435 440 445																
TCT Ser	TCC Ser	ACA Thr	TCG Ser	AAA Lys	TCA Ser	ACC Thr	GGT Gly	GGA Gly	AAG Lys	AGG Arg	TCT Ser	AAC Asn	CGT Arg	AAA Lys	CTC Leu	1392
450 455 460																
TCT Ser	CAT His	CGT Arg	CGT Arg	CGG Arg	TGA *	GACTCTTGCC TCTTAGTGTA ATTTTTGCTG										1440
465 470																
TACCATATAA TTCTGTTTTC ATGATGACTG TAACTGTTTA TGTCTATCGT TGGCGTCATA 1500																
TAGTTTCGCT CTTCGTTTTG CATCCTGTGT ATTATTGCTG CAGGTGTGCT TCAAACAAAT 1560																
GTTGTAACAA TTTGAACCAA TGGTATACAG ATTTGTA 1597																

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 470 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

[illegible]

	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

	55					60					65					
CTT	GTT	CTC	TCC	GAC	GGC	CGG	GAA	GTT	TCT	TTC	CAC	CGG	TGC	GTT	TTG	294
Leu	Val	Leu	Ser	Asp	Gly	Arg	Glu	Val	Ser	Phe	His	Arg	Cys	Val	Leu	
	70					75					80					
TCA	GCG	AGA	AGC	TCT	TTC	TTC	AAG	AGC	GCT	TTA	GCC	GCC	GCT	AAG	AAG	342
Ser	Ala	Arg	Ser	Ser	Phe	Phe	Lys	Ser	Ala	Leu	Ala	Ala	Ala	Lys	Lys	
	85				90					95					100	
GAG	AAA	GAC	TCC	AAC	AAC	ACC	GCC	GCC	GTG	AAG	CTC	GAG	CTT	AAG	GAG	390
Glu	Lys	Asp	Ser	Asn	Asn	Thr	Ala	Ala	Val	Lys	Leu	Glu	Leu	Lys	Glu	
				105					110					115		
ATT	GCC	AAG	GAT	TAC	GAA	GTC	GGT	TTC	GAT	TCG	GTT	GTG	ACT	GTT	TTG	438
Ile	Ala	Lys	Asp	Tyr	Glu	Val	Gly	Phe	Asp	Ser	Val	Val	Thr	Val	Leu	
			120					125					130			
GCT	TAT	GTT	TAC	AGC	AGC	AGA	GTG	AGA	CCG	CCG	CCT	AAA	GGA	GTT	TCT	486
Ala	Tyr	Val	Tyr	Ser	Ser	Arg	Val	Arg	Pro	Pro	Pro	Lys	Gly	Val	Ser	
		135					140					145				
GAA	TGC	GCA	GAC	GAG	AAT	TGC	TGC	CAC	GTG	GCT	TGC	CGG	CCG	GCG	GTG	534
Glu	Cys	Ala	Asp	Glu	Asn	Cys	Cys	His	Val	Ala	Cys	Arg	Pro	Ala	Val	
	150					155					160					
GAT	TTC	ATG	TTG	GAG	GTT	CTC	TAT	TTG	GCT	TTC	ATC	TTC	AAG	ATC	CCT	582
Asp	Phe	Met	Leu	Glu	Val	Leu	Tyr	Leu	Ala	Phe	Ile	Phe	Lys	Ile	Pro	
	165				170					175					180	
GAA	TTA	ATT	ACT	CTC	TAT	CAG	AGG	CAC	TTA	TTG	GAC	GTT	GTA	GAC	AAA	630
Glu	Leu	Ile	Thr	Leu	Tyr	Gln	Arg	His	Leu	Leu	Asp	Val	Val	Asp	Lys	
				185					190					195		
GTT	GTT	ATA	GAG	GAC	ACA	TTG	GTT	ATA	CTC	AAG	CTT	GCT	AAT	ATA	TGT	678
Val	Val	Ile	Glu	Asp	Thr	Leu	Val	Ile	Leu	Lys	Leu	Ala	Asn	Ile	Cys	
			200					205					210			
GGT	AAA	GCT	TGT	ATG	AAG	CTA	TTG	GAT	AGA	TGT	AAA	GAG	ATT	ATT	GTC	726
Gly	Lys	Ala	Cys	Met	Lys	Leu	Leu	Asp	Arg	Cys	Lys	Glu	Ile	Ile	Val	
	215					220						225				
AAG	TCT	AAT	GTA	GAT	ATG	GTT	AGT	CTT	GAA	AAG	TCA	TTG	CCG	GAA	GAG	774
Lys	Ser	Asn	Val	Asp	Met	Val	Ser	Leu	Glu	Lys	Ser	Leu	Pro	Glu	Glu	
	230					235					240					
CTT	GTT	AAA	GAG	ATA	ATT	GAT	AGA	CGT	AAA	GAG	CTT	GGT	TTG	GAG	GTA	822
Leu	Val	Lys	Glu	Ile	Ile	Asp	Arg	Arg	Lys	Glu	Leu	Gly	Leu	Glu	Val	
	245				250					255					260	
CCT	AAA	GTA	AAG	AAA	CAT	GTC	TCG	AAT	GTA	CAT	AAG	GCA	CTT	GAC	TCG	870
Pro	Lys	Val	Lys	Lys	His	Val	Ser	Asn	Val	His	Lys	Ala	Leu	Asp	Ser	
				265					270					275		
GAT	GAT	ATT	GAG	TTA	GTC	AAG	TTG	CTT	TTG	AAA	GAG	GAT	CAC	ACC	AAT	918
Asp	Asp	Ile	Glu	Leu	Val	Lys	Leu	Leu	Leu	Lys	Glu	Asp	His	Thr	Asn	
			280					285					290			
CTA	GAT	GAT	GCG	TGT	GCT	CTT	CAT	TTC	GCT	GTT	GCA	TAT	TGC	AAT	GTG	966
Leu	Asp	Asp	Ala	Cys	Ala	Leu	His	Phe	Ala	Val	Ala	Tyr	Cys	Asn	Val	
	295					300						305				
AAG	ACC	GCA	ACA	GAT	CTT	TTA	AAA	CTT	GAT	CTT	GCC	GAT	GTC	AAC	CAT	1014
Lys	Thr	Ala	Thr	Asp	Leu	Leu	Lys	Leu	Asp	Leu	Ala	Asp	Val	Asn	His	
	310					315					320					

AGG AAT CCG AGG GGA TAT ACG GTG CTT CAT GTT GCT GCG ATG CGG AAG	1062
Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg Lys	
325 330 335 340	
GAG CCA CAA TTG ATA CTA TCT CTA TTG GAA AAA GGT GCA AGT GCA TCA	1110
Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala Ser	
345 350 355	
GAA GCA ACT TTG GAA GGT AGA ACC GCA CTC ATG ATC GCA AAA CAA GCC	1158
Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile Ala Lys Gln Ala	
360 365 370	
ACT ATG GCG GTT GAA TGT AAT AAT ATC CCG GAG CAA TGC AAG CAT TCT	1206
Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln Cys Lys His Ser	
375 380 385	
CTC AAA GGC CGA CTA TGT GTA GAA ATA CTA GAG CAA GAA GAC AAA CGA	1254
Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln Glu Asp Lys Arg	
390 395 400	
GAA CAA ATT CCT AGA GAT GTT CCT CCC TCT TTT GCA GTG GCG GCC GAT	1302
Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala Val Ala Ala Asp	
405 410 415 420	
GAA TTG AAG ATG ACG CTG CTC GAT CTT GAA AAT AGA GTT GCA CTT GCT	1350
Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg Val Ala Leu Ala	
425 430 435	
CAA CGT CTT TTT CCA ACG GAA GCA CAA GCT GCA ATG GAG ATC GCC GAA	1398
Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met Glu Ile Ala Glu	
440 445 450	
ATG AAG GGA ACA TGT GAG TTC ATA GTG ACT AGC CTC GAG CCT GAC CGT	1446
Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp Arg	
455 460 465	
CTC ACT GGT ACG AAG AGA ACA TCA CCG GGT GTA AAG ATA GCA CCT TTC	1494
Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro Phe	
470 475 480	
AGA ATC CTA GAA GAG CAT CAA AGT AGA CTA AAA GCG CTT TCT AAA ACC	1542
Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala Leu Ser Lys Thr	
485 490 495 500	
GTG GAA CTC GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC GAC	1590
Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu Asp	
505 510 515	
CAG ATT ATG AAC TGT TGA	1608
Gln Ile Met Asn Cys *	
520	

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 522 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTG GCT TTC ATC TTC AAG ATC CCT GAA TTA ATT ACT CTC TAT CAG AGG Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile Thr Leu Tyr Gln Arg 50 55 60	192
CAC TTA TTG GAC GTT GTA GAC AAA GTT GTT ATA GAG GAC ACA TTG GTT His Leu Leu Asp Val Val Asp Lys Val Val Ile Glu Asp Thr Leu Val 65 70 75 80	240
ATA CTC AAG CTT GCT AAT ATA TGT GGT AAA GCT TGT ATG AAG CTA TTG Ile Leu Lys Leu Ala Asn Ile Cys Gly Lys Ala Cys Met Lys Leu Leu 85 90 95	288
GAT AGA TGT AAA GAG ATT ATT GTC AAG TCT AAT GTA GAT ATG GTT AGT Asp Arg Cys Lys Glu Ile Ile Val Lys Ser Asn Val Asp Met Val Ser 100 105 110	336
CTT GAA AAG TCA TTG CCG GAA GAG CTT GTT AAA GAG ATA ATT GAT AGA Leu Glu Lys Ser Leu Pro Glu Glu Leu Val Lys Glu Ile Ile Asp Arg 115 120 125	384
CGT AAA GAG CTT GGT TTG GAG GTA CCT AAA GTA AAG AAA CAT GTC TCG Arg Lys Glu Leu Gly Leu Glu Val Pro Lys Val Lys Lys His Val Ser 130 135 140	432
AAT GTA CAT AAG GCA CTT GAC TCG GAT GAT ATT GAG TTA GTC AAG TTG Asn Val His Lys Ala Leu Asp Ser Asp Asp Ile Glu Leu Val Lys Leu 145 150 155 160	480
CTT TTG AAA GAG GAT CAC ACC AAT CTA GAT GAT GCG TGT GCT CTT CAT Leu Leu Lys Glu Asp His Thr Asn Leu Asp Asp Ala Cys Ala Leu His 165 170 175	528
TTC GCT GTT GCA TAT TGC AAT GTG AAG ACC GCA ACA GAT CTT TTA AAA Phe Ala Val Ala Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Leu Lys 180 185 190	576
CTT GAT CTT GCC GAT GTC AAC CAT AGG AAT CCG AGG GGA TAT ACG GTG Leu Asp Leu Ala Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val 195 200 205	624
CTT CAT GTT GCT GCG ATG CGG AAG GAG CCA CAA TTG ATA CTA TCT CTA Leu His Val Ala Ala Met Arg Lys Glu Pro Gln Leu Ile Leu Ser Leu 210 215 220	672
TTG GAA AAA GGT GCA AGT GCA TCA GAA GCA ACT TTG GAA GGT AGA ACC Leu Glu Lys Gly Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr 225 230 235 240	720
GCA CTC ATG ATC GCA AAA CAA GCC ACT ATG GCG GTT GAA TGT AAT AAT Ala Leu Met Ile Ala Lys Gln Ala Thr Met Ala Val Glu Cys Asn Asn 245 250 255	768
ATC CCG GAG CAA TGC AAG CAT TCT CTC AAA GGC CGA CTA TGT GTA GAA Ile Pro Glu Gln Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu 260 265 270	816
ATA CTA GAG CAA GAA GAC AAA CGA GAA CAA ATT CCT AGA GAT GTT CCT Ile Leu Glu Gln Glu Asp Lys Arg Glu Gln Ile Pro Arg Asp Val Pro 275 280 285	864
CCC TCT TTT GCA GTG GCG GCC GAT GAA TTG AAG ATG ACG CTG CTC GAT Pro Ser Phe Ala Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp 290 295 300	912

CTT GAA AAT AGA GTT GCA CTT GCT CAA CGT CTT TTT CCA ACG GAA GCA	960
Leu Glu Asn Arg Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala	
305 310 315 320	
CAA GCT GCA ATG GAG ATC GCC GAA ATG AAG GGA ACA TGT GAG TTC ATA	1008
Gln Ala Ala Met Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile	
325 330 335	
GTG ACT AGC CTC GAG CCT GAC CGT CTC ACT GGT ACG AAG AGA ACA TCA	1056
Val Thr Ser Leu Glu Pro Asp Arg Leu Thr Gly Thr Lys Arg Thr Ser	
340 345 350	
CCG GGT GTA AAG ATA GCA CCT TTC AGA ATC CTA GAA GAG CAT CAA AGT	1104
Pro Gly Val Lys Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser	
355 360 365	
AGA CTA AAA GCG CTT TCT AAA ACC GTG GAA CTC GGG AAA CGA TTC TTC	1152
Arg Leu Lys Ala Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe	
370 375 380	
CCG CGC TGT TCG GCA GTG CTC GAC CAG ATT ATG AAC TGT TGA	1194
Pro Arg Cys Ser Ala Val Leu Asp Gln Ile Met Asn Cys *	
385 390 395	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Asp	Ser	Val	Val	Thr	Val	Leu	Ala	Tyr	Val	Tyr	Ser	Ser	Arg	Val
1				5					10					15	
Arg	Pro	Pro	Pro	Lys	Gly	Val	Ser	Glu	Cys	Ala	Asp	Glu	Asn	Cys	Cys
			20					25					30		
His	Val	Ala	Cys	Arg	Pro	Ala	Val	Asp	Phe	Met	Leu	Glu	Val	Leu	Tyr
		35				40					45				
Leu	Ala	Phe	Ile	Phe	Lys	Ile	Pro	Glu	Leu	Ile	Thr	Leu	Tyr	Gln	Arg
50					55					60					
His	Leu	Leu	Asp	Val	Val	Asp	Lys	Val	Val	Ile	Glu	Asp	Thr	Leu	Val
65				70					75					80	
Ile	Leu	Lys	Leu	Ala	Asn	Ile	Cys	Gly	Lys	Ala	Cys	Met	Lys	Leu	Leu
			85					90					95		
Asp	Arg	Cys	Lys	Glu	Ile	Ile	Val	Lys	Ser	Asn	Val	Asp	Met	Val	Ser
		100						105					110		
Leu	Glu	Lys	Ser	Leu	Pro	Glu	Glu	Leu	Val	Lys	Glu	Ile	Ile	Asp	Arg
		115				120						125			
Arg	Lys	Glu	Leu	Gly	Leu	Glu	Val	Pro	Lys	Val	Lys	Lys	His	Val	Ser
	130				135						140				
Asn	Val	His	Lys	Ala	Leu	Asp	Ser	Asp	Asp	Ile	Glu	Leu	Val	Lys	Leu
145				150					155						160

Leu Leu Lys Glu Asp His Thr Asn Leu Asp Asp Ala Cys Ala Leu His
165 170 175

Phe Ala Val Ala Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Leu Lys
180 185 190

Leu Asp Leu Ala Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val
195 200 205

Leu His Val Ala Ala Met Arg Lys Glu Pro Gln Leu Ile Leu Ser Leu
210 215 220

Leu Glu Lys Gly Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr
225 230 235 240

Ala Leu Met Ile Ala Lys Gln Ala Thr Met Ala Val Glu Cys Asn Asn
245 250 255

Ile Pro Glu Gln Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu
260 265 270

Ile Leu Glu Gln Glu Asp Lys Arg Glu Gln Ile Pro Arg Asp Val Pro
275 280 285

Pro Ser Phe Ala Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp
290 295 300

Leu Glu Asn Arg Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala
305 310 315 320

Gln Ala Ala Met Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile
325 330 335

Val Thr Ser Leu Glu Pro Asp Arg Leu Thr Gly Thr Lys Arg Thr Ser
340 345 350

Pro Gly Val Lys Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser
355 360 365

Arg Leu Lys Ala Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe
370 375 380

Pro Arg Cys Ser Ala Val Leu Asp Gln Ile Met Asn Cys *
385 390 395

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..786
 - (D) OTHER INFORMATION: /product= "Altered form of NIM1"
- /note= "Ankyrin domains of NIM1."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATG GAC TCC AAC AAC ACC GCC GCC GTG AAG CTC GAG CTT AAG GAG ATT	48
Met Asp Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu Ile	
1 5 10 15	
GCC AAG GAT TAC GAA GTC GGT TTC GAT TCG GTT GTG ACT GTT TTG GCT	96
Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu Ala	
20 25 30	
TAT GTT TAC AGC AGC AGA GTG AGA CCG CCG CCT AAA GGA GTT TCT GAA	144
Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser Glu	
35 40 45	
TGC GCA GAC GAG AAT TGC TGC CAC GTG GCT TGC CGG CCG GCG GTG GAT	192
Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp	
50 55 60	
TTC ATG TTG GAG GTT CTC TAT TTG GCT TTC ATC TTC AAG ATC CCT GAA	240
Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu	
65 70 75 80	
TTA ATT ACT CTC TAT CAG AGG CAC TTA TTG GAC GTT GTA GAC AAA GTT	288
Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp Val Val Asp Lys Val	
85 90 95	
GTT ATA GAG GAC ACA TTG GTT ATA CTC AAG CTT GCT AAT ATA TGT GGT	336
Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile Cys Gly	
100 105 110	
AAA GCT TGT ATG AAG CTA TTG GAT AGA TGT AAA GAG ATT ATT GTC AAG	384
Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile Val Lys	
115 120 125	
TCT AAT GTA GAT ATG GTT AGT CTT GAA AAG TCA TTG CCG GAA GAG CTT	432
Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu Glu Leu	
130 135 140	
GTT AAA GAG ATA ATT GAT AGA CGT AAA GAG CTT GGT TTG GAG GTA CCT	480
Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu Val Pro	
145 150 155 160	
AAA GTA AAG AAA CAT GTC TCG AAT GTA CAT AAG GCA CTT GAC TCG GAT	528
Lys Val Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp Ser Asp	
165 170 175	
GAT ATT GAG TTA GTC AAG TTG CTT TTG AAA GAG GAT CAC ACC AAT CTA	576
Asp Ile Glu Leu Val Lys Leu Leu Leu Lys Glu Asp His Thr Asn Leu	
180 185 190	
GAT GAT GCG TGT GCT CTT CAT TTC GCT GTT GCA TAT TGC AAT GTG AAG	624
Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn Val Lys	
195 200 205	
ACC GCA ACA GAT CTT TTA AAA CTT GAT CTT GCC GAT GTC AAC CAT AGG	672
Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn His Arg	
210 215 220	
AAT CCG AGG GGA TAT ACG GTG CTT CAT GTT GCT GCG ATG CCG AAG GAG	720
Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg Lys Glu	
225 230 235 240	
CCA CAA TTG ATA CTA TCT CTA TTG GAA AAA GGT GCA AGT GCA TCA GAA	768
Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala Ser Glu	
245 250 255	

GCA ACT TTG GAA GGT TGA
 Ala Thr Leu Glu Gly *
 260

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 262 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Asp Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu Ile
 1 5 10 15
 Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu Ala
 20 25 30
 Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser Glu
 35 40 45
 Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp
 50 55 60
 Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu
 65 70 75 80
 Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp Val Val Asp Lys Val
 85 90 95
 Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile Cys Gly
 100 105 110
 Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile Val Lys
 115 120 125
 Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu Glu Leu
 130 135 140
 Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu Val Pro
 145 150 155 160
 Lys Val Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp Ser Asp
 165 170 175
 Asp Ile Glu Leu Val Lys Leu Leu Leu Lys Glu Asp His Thr Asn Leu
 180 185 190
 Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn Val Lys
 195 200 205
 Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn His Arg
 210 215 220
 Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg Lys Glu
 225 230 235 240
 Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala Ser Glu
 245 250 255
 Ala Thr Leu Glu Gly *

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Ile Arg Arg Met Arg Arg Ala Leu Asp Ala Ala Asp Ile Glu Leu Val
1           5           10           15
Lys Leu Met Val Met Gly Glu Gly Leu Asp Leu Asp Asp Ala Leu Ala
          20           25           30
Val His Tyr Ala Val Gln His Cys Asn
          35           40

```

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

Pro Thr Gly Lys Thr Ala Leu His Leu Ala Ala Glu Met Val Ser Pro
1           5           10           15
Asp Met Val Ser Val Leu Leu Asp His His Ala Asp Xaa Asn Phe Arg
          20           25           30
Thr Xaa Asp Gly Val Thr
          35

```

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile Arg Arg Met Arg Arg Ala Leu Asp Ala Ala Asp Ile Glu Leu Val
 1 5 10 15
 Lys Leu Met Val Met Gly Glu Gly Leu Asp Leu Asp Asp Ala Leu Ala
 20 25 30
 Val His Tyr Ala Val Gln His Cys Asn
 35 40

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg Arg Pro Asp Ser Lys Thr Ala Leu His Leu Ala Ala Glu Met Val
 1 5 10 15
 Ser Pro Asp Met Val Ser Val Leu Leu Asp Gln
 20 25

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ile Arg Arg Met Arg Arg Ala Leu Asp Ala Ala Asp Ile Glu Leu Val
 1 5 10 15
 Lys Leu Met Val Met Gly Glu Gly Leu Asp Leu Asp Asp Ala Leu Ala
 20 25 30
 Val His Tyr Ala Val Gln His Cys Asn
 35 40

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Arg Arg Pro Asp Ser Lys Thr Ala Leu His Leu Ala Ala Glu Met Val
1 5 10 15
Ser Pro Asp Met Val Ser Val Leu Leu Asp Gln
20 25

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ile Arg Arg Met Arg Arg Ala Leu Asp Ala Ala Asp Ile Glu Leu Val
1 5 10 15
Lys Leu Met Val Met Gly Glu Gly Leu Asp Leu Asp Asp Ala Leu Ala
20 25 30
Val His Tyr Ala Val Gln His Cys Asn
35 40

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Pro Thr Gly Lys Thr Ala Leu His Leu Ala Ala Glu Met Val Ser Pro
1 5 10 15
Asp Met Val

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAACAGCTTC GAAGCCGTCT TTGACGCGCC GGATG

35

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CATCCGGCGC GTCAAAGACG GCTTCGAAGC TGTTC

35

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGAATTCAAT GGATTGGTT GTGACTGTTT TG

32

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGAATTCTAC AAATCTGTAT ACCATTGG

28

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CGGAATTCGA TCTCTTTAAT TTGTGAATTT C

31

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGAATTCTCA ACAGTTCATA ATCTGGTCG

29

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGAATTCAAT GGACTCCAAC AACACCGCCG C

31

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGAATTCTCA ACCTTCCAAA GTTGCTTCTG ATG

33

TGTTCTCAACCTTCTG